



IFW16

RAW SEQUENCE LISTING

DATE: 07/21/2004

PATENT APPLICATION: US/09/550,163C

TIME: 10:47:47

Input Set : A:\150suppseqlistrev.txt

Output Set: N:\CRF4\07212004\I550163C.raw

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3 <110> APPLICANT: University of Utah Research Foundation
4   Yale University
5   Abbott, Geoffrey W
6   Sesti, Federico
7   Splawski, Igor
8   Keating, Mark T
9   Goldstein, Steve A.N.
11 <120> TITLE OF INVENTION: MinK-Related Genes, Formation of Potassium Channels and
12   Association with Cardiac Arrhythmia
14 <130> FILE REFERENCE: 2323-150.a
16 <140> CURRENT APPLICATION NUMBER: 09/550,163C
17 <141> CURRENT FILING DATE: 2000-04-14
19 <150> PRIOR APPLICATION NUMBER: US 60/129,404
20 <151> PRIOR FILING DATE: 1999-04-15
22 <160> NUMBER OF SEQ ID NOS: 22
23 <170> SOFTWARE: PatentIn version 3.1/2.0
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26 <211> LENGTH: 732
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
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32 <222> LOCATION: (74)..(442)
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37 gcaggaggga agc tct act tta tcc aat ttc aca cag acg ctg gaa 109
38           Met Ser Thr Leu Ser Asn Phe Thr Gln Thr Leu Glu
39           1           5           10
41 gac gtc ttc cga agg att ttt att act tat atg gac aat tgg cgc cag 157
42 Asp Val Phe Arg Arg Ile Phe Ile Thr Tyr Met Asp Asn Trp Arg Gln
43           15           20           25
45 aac aca aca gct gag caa gag gcc ctc caa gcc aaa gtt gat gct gag 205
46 Asn Thr Thr Ala Glu Gln Glu Ala Leu Gln Ala Lys Val Asp Ala Glu
47           30           35           40
49 aac ttc tac tat gtc atc ctg tac ctc atg gtg atg att gga atg ttc 253
50 Asn Phe Tyr Tyr Val Ile Leu Tyr Leu Met Val Met Ile Gly Met Phe
51 45           50           55           60
53 tct ttc atc atc gtg gcc atc ctg gtg agc act gtg aaa tcc aag aga 301
54 Ser Phe Ile Ile Val Ala Ile Leu Val Ser Thr Val Lys Ser Lys Arg
55           65           70           75
57 cgg gaa cac tcc aat gac ccc tac cac cag tac att gta gag gac tgg 349
58 Arg Glu His Ser Asn Asp Pro Tyr His Gln Tyr Ile Val Glu Asp Trp
59           80           85           90

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61 cag gaa aag tac aag agc caa atc ttg aat cta gaa gaa tcg aag gcc 397
62 Gln Glu Lys Tyr Lys Ser Gln Ile Leu Asn Leu Glu Glu Ser Lys Ala
63      95      100      105
65 acc atc cat gag aac att ggt gcg gct ggg ttc aaa atg tcc ccc 442
66 Thr Ile His Glu Asn Ile Gly Ala Ala Gly Phe Lys Met Ser Pro
67      110      115      120
69 tgataaggga gaaaggcacc aagctaacat ctgacgtcca gacatgaaga gatgccagt 502
71 ccacgaggca aatccaaatt gtctttgctt agaagaaagt gagttccttg ctctttgttg 562
73 agaattttca tggagattat gtggttgccc aataaagata gatgacattt caatctcagt 622
75 gatttatgct tgcttggttg agcaatattt tgtgctgaag acctctttta ctttccgggc 682
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87 1      5      10      15
89 Arg Ile Phe Ile Thr Tyr Met Asp Asn Trp Arg Gln Asn Thr Thr Ala
90      20      25      30
92 Glu Gln Glu Ala Leu Gln Ala Lys Val Asp Ala Glu Asn Phe Tyr Tyr
93      35      40      45
95 Val Ile Leu Tyr Leu Met Val Met Ile Gly Met Phe Ser Phe Ile Ile
96      50      55      60
98 Val Ala Ile Leu Val Ser Thr Val Lys Ser Lys Arg Arg Glu His Ser
99 65      70      75      80
101 Asn Asp Pro Tyr His Gln Tyr Ile Val Glu Asp Trp Gln Glu Lys Tyr
102      85      90      95
104 Lys Ser Gln Ile Leu Asn Leu Glu Glu Ser Lys Ala Thr Ile His Glu
105      100      105      110
107 Asn Ile Gly Ala Ala Gly Phe Lys Met Ser Pro
108      115      120
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112 <211> LENGTH: 468
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114 <213> ORGANISM: Rattus norvegicus
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117 <221> NAME/KEY: CDS
118 <222> LOCATION: (35)..(403)
120 <400> SEQUENCE: 3
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122      Met Thr Thr Leu Ala Asn Leu
123      1      5
125 acg cag acc ctg gag gat gcc ttc aaa aag gtt ttc att act tat atg 103
126 Thr Gln Thr Leu Glu Asp Ala Phe Lys Lys Val Phe Ile Thr Tyr Met
127      10      15      20
129 gac agc tgg agg agg aac aca aca gcc gaa caa cag gcg ctc cag gcc 151
130 Asp Ser Trp Arg Arg Asn Thr Thr Ala Glu Gln Gln Ala Leu Gln Ala
131      25      30      35

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133 aga gtg gat gcc gag aac ttc tac tac gtc atc ctg tac ctc atg gtg 199
134 Arg Val Asp Ala Glu Asn Phe Tyr Tyr Val Ile Leu Tyr Leu Met Val
135 40 45 50 55
137 atg atc ggc atg ttc gcc ttc atc gtg gtg gcc atc ctg gtg agc acg 247
138 Met Ile Gly Met Phe Ala Phe Ile Val Val Ala Ile Leu Val Ser Thr
139 60 65 70
141 gtg aag tcg aag cgg cgg gag cac tcc cag gac ccg tac cac cag tac 295
142 Val Lys Ser Lys Arg Arg Glu His Ser Gln Asp Pro Tyr His Gln Tyr
143 75 80 85
145 atc gtg gag gat tgg cag cag aag tat agg agt cag atc ttg cat ctg 343
146 Ile Val Glu Asp Trp Gln Gln Lys Tyr Arg Ser Gln Ile Leu His Leu
147 90 95 100
149 gaa gac tcc aag gcc acc atc cat gag aac ctg ggg gcg acg ggg ttc 391
150 Glu Asp Ser Lys Ala Thr Ile His Glu Asn Leu Gly Ala Thr Gly Phe
151 105 110 115
153 aca gtg tca ccc tgataaagaa cgagagtcca tctgcccagg aaggggtgct 443
154 Thr Val Ser Pro
155 120
157 tctgcccgcct tgaagcccca cttgc 468
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161 <211> LENGTH: 123
162 <212> TYPE: PRT
163 <213> ORGANISM: Rattus norvegicus
165 <400> SEQUENCE: 4
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167 1 5 10 15
169 Lys Val Phe Ile Thr Tyr Met Asp Ser Trp Arg Arg Asn Thr Thr Ala
170 20 25 30
172 Glu Gln Gln Ala Leu Gln Ala Arg Val Asp Ala Glu Asn Phe Tyr Tyr
173 35 40 45
175 Val Ile Leu Tyr Leu Met Val Met Ile Gly Met Phe Ala Phe Ile Val
176 50 55 60
178 Val Ala Ile Leu Val Ser Thr Val Lys Ser Lys Arg Arg Glu His Ser
179 65 70 75 80
181 Gln Asp Pro Tyr His Gln Tyr Ile Val Glu Asp Trp Gln Gln Lys Tyr
182 85 90 95
184 Arg Ser Gln Ile Leu His Leu Glu Asp Ser Lys Ala Thr Ile His Glu
185 100 105 110
187 Asn Leu Gly Ala Thr Gly Phe Thr Val Ser Pro
188 115 120
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192 <211> LENGTH: 492
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194 <213> ORGANISM: Homo sapiens
196 <220> FEATURE:
197 <221> NAME/KEY: CDS
198 <222> LOCATION: (93)..(401)
200 <400> SEQUENCE: 5
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203 cccaggtcttc cccacactca atccctgttg ct atg gag act acc aat gga acg 113
204                               Met Glu Thr Thr Asn Gly Thr
205                               1                               5
207 gag acc tgg tat gag agc ctg cat gcc gtg ctg aag gct cta aat gcc 161
208 Glu Thr Trp Tyr Glu Ser Leu His Ala Val Leu Lys Ala Leu Asn Ala
209          10                      15                      20
211 act ctt cac agc aat ttg ctc tgc cgg cca ggg cca ggg ctg ggg cca 209
212 Thr Leu His Ser Asn Leu Leu Cys Arg Pro Gly Pro Gly Leu Gly Pro
213          25                      30                      35
215 gac aac cag act gaa gag agg cgg gcc agc cta cct ggc cgt gat gac 257
216 Asp Asn Gln Thr Glu Glu Arg Arg Ala Ser Leu Pro Gly Arg Asp Asp
217 40                      45                      50                      55
219 aac tcc tac atg tac att ctc ttt gtc atg ttt cta ttt gct gta act 305
220 Asn Ser Tyr Met Tyr Ile Leu Phe Val Met Phe Leu Phe Ala Val Thr
221          60                      65                      70
223 gtg ggc agc ctc atc ctg gga tac acc cgc tcc cgc aaa gtg gac aag 353
224 Val Gly Ser Leu Ile Leu Gly Tyr Thr Arg Ser Arg Lys Val Asp Lys
225          75                      80                      85
227 cgt agt gac ccc tat cat gtg tat atc aag aac cgt gtg tct atg atc 401
228 Arg Ser Asp Pro Tyr His Val Tyr Ile Lys Asn Arg Val Ser Met Ile
229          90                      95                      100
231 taacacgaga gggctgggac ggtggaagac caagacacct ggggattgcg tctggggcct 461
233 ccagaactct gctgtggact gcacaggtc t 492
236 <210> SEQ ID NO: 6
237 <211> LENGTH: 103
238 <212> TYPE: PRT
239 <213> ORGANISM: Homo sapiens
241 <400> SEQUENCE: 6
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243 1                               5                               10                               15
245 Val Leu Lys Ala Leu Asn Ala Thr Leu His Ser Asn Leu Leu Cys Arg
246          20                      25                      30
248 Pro Gly Pro Gly Leu Gly Pro Asp Asn Gln Thr Glu Glu Arg Arg Ala
249          35                      40                      45
251 Ser Leu Pro Gly Arg Asp Asp Asn Ser Tyr Met Tyr Ile Leu Phe Val
252          50                      55                      60
254 Met Phe Leu Phe Ala Val Thr Val Gly Ser Leu Ile Leu Gly Tyr Thr
255 65                      70                      75                      80
257 Arg Ser Arg Lys Val Asp Lys Arg Ser Asp Pro Tyr His Val Tyr Ile
258          85                      90                      95
260 Lys Asn Arg Val Ser Met Ile
261          100
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267 <213> ORGANISM: Mus musculus
269 <220> FEATURE:
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271 <222> LOCATION: (241)..(549)

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273 <400> SEQUENCE: 7

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276 gagaaacaaa acaccagtgt ttctgtctgt gccatttgg aaccaagaga tgcaccttgc 120
278 aaggaactga ggggttgttg gacatccacg aagagatcct caaagatgtc tcagagccag 180
280 cagagtctct gaactgtttg atcacattcc agctcttccc atacctcaat atctgttgc 240
282 atg gag act tcc aac ggg act gag acc tgg tac atg agc ctc cat gct 288
283 Met Glu Thr Ser Asn Gly Thr Glu Thr Trp Tyr Met Ser Leu His Ala
284 1 5 10 15
286 gtg ctg aag gct ctg aac aca acc ctt cac agt cac ttg ctc tgc cgg 336
287 Val Leu Lys Ala Leu Asn Thr Thr Leu His Ser His Leu Leu Cys Arg
288 20 25 30
290 cct ggg cca gga cca ggg cca gac aat caa act gag gat cgt cgg gct 384
291 Pro Gly Pro Gly Pro Gly Pro Asp Asn Gln Thr Glu Asp Arg Arg Ala
292 35 40 45
294 agc ctt cct ggt cgt aat gac aac tcc tac atg tat att ctc ttt gtc 432
295 Ser Leu Pro Gly Arg Asn Asp Asn Ser Tyr Met Tyr Ile Leu Phe Val
296 50 55 60
298 atg ttc cta ttt gcc gtc act gtg ggc agt ctc atc ctg gga tat acc 480
299 Met Phe Leu Phe Ala Val Thr Val Gly Ser Leu Ile Leu Gly Tyr Thr
300 65 70 75 80
302 cgt tca cgc aaa gtg gac aaa cgt agt gac ccc tat cat gtg tac atc 528
303 Arg Ser Arg Lys Val Asp Lys Arg Ser Asp Pro Tyr His Val Tyr Ile
304 85 90 95
306 aag aac cgt gtg tct atg atc tgatgtgagg aacctgaaga caatggaaga 579
307 Lys Asn Arg Val Ser Met Ile
308 100
310 ttacaatgtc tgaggattgt cttctggtgc ctccggaact caactcaacc atatcaagcc 639
312 acagtgtatc tatgtaagat caacaggaaa ctggtaagag gattaggtca ttattaggac 699
314 cagagaagag ggactgatag gccagctctt gtggatgaga cttttttcga gacacagatg 759
316 cgcattataa actcagagcc catgaacaca tatatataaa gtatggacaa ccagcaagta 819
318 gaagaggaag ctgtggcgaa gggaaatggg gcagaaagat gctctggata tataatcttt 879
320 taatgtatga tcttcaacat gagaaacctt gataaaactg agaatgctac ttaaaaaaaa 939
322 aaaaaaaaaa aaaaaaattt ccgcggccgc aag 972

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325 <210> SEQ ID NO: 8

326 <211> LENGTH: 103

327 <212> TYPE: PRT

328 <213> ORGANISM: Mus musculus

330 <400> SEQUENCE: 8

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334 Val Leu Lys Ala Leu Asn Thr Thr Leu His Ser His Leu Leu Cys Arg
335 20 25 30
337 Pro Gly Pro Gly Pro Gly Pro Asp Asn Gln Thr Glu Asp Arg Arg Ala
338 35 40 45
340 Ser Leu Pro Gly Arg Asn Asp Asn Ser Tyr Met Tyr Ile Leu Phe Val
341 50 55 60
343 Met Phe Leu Phe Ala Val Thr Val Gly Ser Leu Ile Leu Gly Tyr Thr
344 65 70 75 80
346 Arg Ser Arg Lys Val Asp Lys Arg Ser Asp Pro Tyr His Val Tyr Ile

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VERIFICATION SUMMARY

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